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A GIS-based multi-criteria evaluation approach to map Rift Valley fever risk areas in Europe

> **A. Tran** [1,2], C. Ippoliti [3], M. Gely [1], T. Balenghien [4], A. Conte [3], T. Baldet [4], M. Goffredo [3], P. Calistri [3], C. Chevalier [1]

[1] Cirad, UR Animal et Gestion Intégrée des Risques (AGIR), Montpellier, France
[2] Cirad, Territoires, Environnement, Télédétection et Information Spatiale (TETIS) (UMR AgroParisTech-Cirad-Irstea), Montpellier, France
[3] Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise 'G. Caporale', Teramo, Italia
[4] Cirad, Contrôle des maladies animales exotiques et emergentes (CMAEE) (UMR Cirad-Inra), Montpellier, France

Rift Valley fever (RVF) is a severe mosquito-borne disease affecting domestic ruminants and humans, caused by a Phlebovirus (Bunyaviridae). RVF virus (RVFV) infection may result either from mosquito bites or contact with a viremic animal, or exposure to body fluids. Recently its distribution enlarged, threatening northern Africa, a large outbreak occurred in northern Mauritania in 2010, Middle East and Europe. Even if the probability of introduction and large-scale spread of RVFV in Europe is very low, localized RVF outbreaks may occur in areas where population of ruminants and potential vectors are present.

The goal of this study was to identify European suitable areas for RVF transmission. We focused on the risk of transmission of RVFV to three main European potential hosts, i.e. cattle, sheep and goats, considering only the vectorial transmission. Very few is known about European mosquito competency. Based on a literature review, five mosquito species belonging to *Culex* and *Aedes* genera, present in Europe and likely to play a role in RVFV transmission in case of virus introduction were identified: *Culex (Culex) pipiens, Culex (Culex) theileri, Aedes (Aedimorphus) vexans vexans, Aedes (Ochlerotatus) caspius* and *Aedes (Stegomyia) albopictus*. We first modelled the geographic distribution of each of these five species, based on expert knowledge and using land cover (Corine Land cover database) and elevation as proxy of mosquito presence. Then, the risk of RVFV transmission was modelled using a Multi-Criteria Evaluation (MCE) approach, integrating available experimental data on vector competence, expert knowledge on abundance, host density data and literature knowledge on host sensitivity. A sensitivity analysis was performed to assess the robustness of the results with respect to expert choices in the selection, weights assignments and combination of the different factors.

The resulting maps include *i)* five maps of vector distribution, one for each potential vector species; *ii)* a map of suitable areas for vectorial transmission of RVFV considering the presence of at least one of the five mosquito species, their potential competency and abundance; and *iii)* a map of the risk of vector-borne transmission to cattle, sheep and goats. As expected, the resulting RVFV risk maps highlighted a strong spatial heterogeneity throughout Europe. For validation, mosquito distribution maps were compared to mosquito collection data from Italy, showing a good agreement between modelled presence probability and observed presence or absence of each species. The same validation should be performed for other European countries, at least distinguishing the main European regions, i.e. Southern, Northern and Eastern Europe. Additionally, and as far as Africa is concerned, it is well known that sheep are more sensitive than goats that are themselves more sensitive than cattle. In the absence of contradictory evidence for Europe, we considered that the three main hosts were equally sensitive to the virus. This assumption need to be validated by laboratory experiments. Lastly, we did not take into account the direct transmission which is supposed to substantially support the transmission during outbreaks in Africa. The next step could be to improve this model including a direct transmission term when available.

As conclusion, we found that MCE offered a valuable framework and flexible tool for the mapping of areas at risk for the transmission of a pathogen which is absent from a region. It helped identifying gaps in knowledge of the transmission of RVFV in Europe. In particular, further lab experiments are needed - as very little is known about the competence of mosquito European species, we used estimations available for African species to estimate the role of each species as potential vectors, but this extrapolation is uncertain. Given the absence of relevant models for Europe, the cost of active surveillance and the numerous potential entry ways for the virus, the surveillance of RVF in Europe will be challenging in the next coming years. In the future, additional relevant geographic information on animal trade and importations could be integrated to refine these first risk maps and use them to target RVF surveillance in Europe.